

1	cgagaaaaggtgacgcggggcccgggcaggcgccggcgccggcccccccccccccg	
61	cctgggtatttggccgccttcgcccgcagctcagggcagagtctcctggaaggcgaggc	
121	agtgtggcgagaagggcgctgtgttctttcttttctgtctttcccccggttgccg	
181	ctggaagctgcgcgcgagttcctgcaaggcggtctgccgcggccggggcccgcttctc	
241	ccctcgagcgaccccgctcgccggcgccggggcccgaggtagcccgaggcgccggag	
301	gagccagccccagcgagcgccgggagaggcgccagcgagccggacgcacagcgagcgg	
361	gccggcaccagctcgccggggcccgactcggaactcgccggcgccggcgccggcccg	
421	cccagcgaggggtggggggcgccggcgccggcgccggg	
457	cgccggcgagcgggggccATGCAGGCGCGCTACTCCGTGTCCAGCCCCAACTCC	
	.....METGlnAlaArgTyrSerValSerSerProAsnSer	12
511	CTGGGAGTGGTGCCCTACCTCGGCGGCGAGCAGAGCTACTACCGCGCGGCGGCC	
	LeuGlyValValProTyrLeuGlyGlyGluGlnSerTyrTyrArgAlaAlaAla	30
565	GCGGCGGCGCGGGGCGGCTACACCGCCATGCCGCCCCCATGAGCGTGTACTCG	
	AlaAlaAlaGlyGlyGlyTyrThrAlaMETProAlaProMETSerValTyrSer	48
619	CACCTGCGCACGCCGAGCAGTACCCGGGCGGCATGGCCCGCGCCTACGGGCCC	
	HisProAlaHisAlaGluGlnTyrProGlyGlyMETAlaArgAlaTyrGlyPro	66
673	TACACGCCGCGAGCCGAGCCCAAGGACATGGTGAAGCCGCCCTATAGCTACATC	
	TyrThrProGlnProGlnProLysAspMETValLysProProTyrSerTyrIle	84
727	GCGCTCATCACCATGGCCATCCAGAACGCCCCGACAAGAAGATCACCTGAAC	
	AlaLeuIleThrMETAlaIleGlnAsnAlaProAspLysLysIleThrLeuAsn	102
781	GGCATCTACCAATTATCATGGACCGCTTCCCTTCTACCGGGACAACAAGCAG	
	GlyIleTyrGlnPheIleMETAspArgPheProPheTyrArgAspAsnLysGln	120
835	GGCTGGCAGAACAGCATCCGCCACAACCTCTCGCTCAACGAGTGCTTCGTCAAG	
	GlyTrpGlnAsnSerIleArgHisAsnLeuSerLeuAsnGluCysPheValLys	138
889	GTGCCGCGCAGCACAAGAAGCCGGGCAAGGGCAGCTACTGGACGCTGGACCCG	
	ValProArgAspAspLysLysProGlyLysGlySerTyrTrpThrLeuAspPro	156
943	GA CTCTACAACATGTTTCGAGAACGGCAGCTTCCTGCGGCGGCGGCGGCTTC	
	AspSerTryAsnMETPheGluAsnGlySerPheLeuArgArgArgArgPhe	174
997	AAGAAGAAGGACCGGTGAAGGACAAGGAGGAGAAGGACAGGCTGCACCTCAAG	
	LysLysLysAspAlaValLysAspLysGluGluLysAspArgLeuHisLeuLys	192
1051	GAGCCGCCCCCGCCGCGCCAGCCCCCGCCGCGCGCGGAGCAGGCCGAC	
	GluProProProProGlyArgGlnProProProAlaProProGluGlnAlaAsp	210
1105	GGCAACGCGCCCGGTCCGCAGCCCGCCCGTGGCATCCAGGACATCAAGACC	
	GlyAsnAlaProGlyProGlnProProProValArgIleGlnAspIleLysThr	228
1159	GAGAACGGTACGTGCCCCCTCGCCGCCCCAGCCCCCTGTCCCCGCGCGCCGCTG	
	GluAsnGlyThrCysProSerProProGlnProLeuSerProAlaAlaAlaLeu	246
1213	GGCAGCGGACGCGCCCGCGGTGCCCAAGATCGAGAGCCCCGACAGCAGCAGC	
	GlySerGlySerAlaAlaAlaValProLysIleGluSerProAspSerSerSer	264
1267	AGCAGCCTGTCCAGCGGGAGCAGCCCCCGGGCAGCCTGCCGTGCGCGCGGCCG	
	SerSerLeuSerSerGlySerSerProProGlySerLeuProSerAlaArgPro	282
1321	CTCAGCCTGGACGGTGCGGATTCCGCGCCGCGCCGCGCCGCGCCCTCCGCCCCG	
	LeuSerLeuAspGlyAlaAspSerAlaProProProProAlaProSerAlaPro	300
1375	CCGCCGACCATAGCCAGGGCTTCAGCGTGGACAACATCATGACGTGCGTGGCG	
	ProProHisHisSerGlnGlyPheSerValAspAsnIleMETThrSerLeuArg	318
1429	GGGTGCGCGCAGAGCGCGCGCGGAGCTCAGCTCCGGCCTTCTGGCCTCGGCG	
	GlySerProGlnSerAlaAlaAlaGluLeuSerSerGlyLeuLeuAlaSerAla	336
1483	GCCGCGTCTCGCGCGCGGGGATCGCACCCCGCTGGCGCTCGGCGCCTACTCG	
	AlaAlaSerSerArgAlaGlyIleAlaProProLeuAlaLeuGlyAlaTyrSer	354
1537	CCCGGCCAGAGCTCCCTCTACAGCTCCCCCTGCAGCCAGACCTCCAGCGCGGGC	
	ProGlyGlnSerSerLeuTyrSerSerProCysSerGlnThrSerSerAlaGly	372

Fig. 1A

[illegible]

Fig. 1B

	Helix 1	Helix 2	Helix 3	Wing 1	Wing 2
Forkhead SYTHA.....	S.....N.TRML.SE.....L.....Q.Q.R.....S.F.D.....I.TPD.....F.HL...G.....CY...QK...CDK				
FKHL7	PKDVKPPSYIALITHAIQADKKITINGIYQFIMDRFFYDNKQGWQNSIRHNLNSNECFVKYPRDDKXPGKGSYTWLDPDSYNMFENGSLRRRRRFFKKKD				
Mutations					
		S	M	L	
FKHL14	...L.....E.....E.....				
FKHL18	TTBPT.....A...SS.GQRA.S...RV.G.A.A.H.RP.....			R.....	CHD...H.....TRQT
FKHL11	AETPQ.....A...D.EQRV.....			H.R.....	EKGR.....RCLD...N.YR.K.KP.PGP
FKHL12	LQRG.....A.LAH.GRRL.AA.R.TE.A...SPRK.....			T.D.....	EPGN...N...AAAD.D...P.K...RAE
FKHL15	LQRG.....A.AH.ERR.L.G.K.TE.....			PKK.....	T.D.L.I.EAGR...N.A.NAED...S...K...RS.
FKHL9	ARQPA...S.....LQS.H.R.L.S.CA.S...Y.RKFP.....			D...I.EPGR...N.S.A.QD.D...K.QRNQ	
FKHL8	ETRL.....LQS.K.R.L.S.E.CE.SG...Y.EKFP.....			D...I.EPGR...N.E.AD.D...K.RQP	
FKHL17	RSPL.....LQS.KKRL.S.E.CE.SG...Y.EKFP.....			D...I.EPGR...N.E.AD.D...K.RQP	
FKHL5	IRRPE.....V...SS.T.R.L.SE.....LQS...F.GSY...K.V.....			I.L.KGLGR...H.I.A.EF...R...G.RR.C	
FKHL6	LRRPE.....V...SS.S.R.L.SE.....LQA...F.GAY...K.V.....			I.L.KGLGR...H.I.A.EF...R...G.RR.C	
FKHL4	NGKYE...F.N.M.RQS.E.R.L.....E.KN.Y.E.....			HYDD...N.M.S.DDV.IG.TTGKL...STTSP	
FKHL2	NGKYE...F.N.M.MEQS.E.R.L.....E.KN.Y.E.....			HYDD...N.M.S.DDV.IG.TTGKL...STTSPA	
FKHL3	G.YEKP...F.N.M.RQS.E.R.L.....E.KN.Y.E...H...D...K.....			HYDD...N.M.S.DDV.IG.TTGKL...STTSR	
FKHL10	LMKLVR.....S.A.HG...R.L.SQ...YVA.N...NKS.A.....			D.K.....	EDD...
FKHL13	TNPH.....AT.C.M.ASKAT...SA.KW.T.N.CYF.HADPT.....			K.I.....	EKDE....GF.RI.QYAERLLS.AFKK..LPFVHIH
FKHR	WGNLSYADLITK.IESS.EKRLTILSQ.YEWMVKSVYFKDKGDSNSA..K.....			HSK.IR.QNEGTKSSWMMLNPEGGKSGKSPRRAASMD	

Fig. 2

Clone Name	Image Number	Organism	Vector	Loc	5' Sequence	3' Sequence	Insert Size	Tissue	Contig
zr45a08	666326	Human		3'	AA232742	AA232201		NHMPu	
zw04a06	768274	Human		3'		AA424787		NHMPu	
zv90g12	767110	Human		3'	AA424381	AA424466		NHMPu	
yw76b12	258143	Human	pT7T3D	3'	N40575			Placenta, 8 to 9 wk	
zel3t07	358885	Human		3'		W94629		Fetal Heart	
yw78d12	258359	Human		3'		N25875		Placenta, 8 to 9 wk	
zw05a06	768370	Human	pT7T3D	3'	AA495846		722	NHMPu	
oj36t08	1500423	Human		3'		AA885880		NCI CGAP_Lu5	
zd71b11	346077	Human		3'	W77980			Fetal Heart, 19 wk	
ah14c11	1156628	Human		3'		AA776534		Wilms Tumor	
oh48b09	1469849	Human		3'		AA865139		NCI CGAP_GC4	
zd71b12	346079	Human		3'		W73917		Fetal Heart, 19 wk	
ze71a01	364392	Human	pT7T3D	3'	AA022618	AA022755	919	Fetal Heart, 19 wk	
zel3t07	358885	Human		3'	W94714			Fetal Heart, 19 wk	
ok90g07	1521276	Human		3'		AA902429		Fetal Heart, 19 wk	
yw78b12	258335	Human		3'		N25867		NCI CGAP_Lu5	
yw28c11	253556	Human	pBlue SK-	3'	H89575			Placenta, 8 to 9 wk	
EST54452		Human		3'	AA348051			Fetal Cochlea	
EST38957		Human		3'	AA334694			Fetal Heart	
yw30d03	253733	Human	pBlue SK-	3'	N75774	N22552	475	Embryo, 9 wk	
nj57a04	996558	Human		3'	AA551599			Fetal Cochlea	
yw76d12	258167	Human	pT7T3D	3'	N40582			NCI CGAP_Pr9	
nv16g07	1220412	Human		3'		AA688135		Placenta, 8 to 9 wk	
GEN-206f07		Human		3'	D56550			NCI CGAP_Pr22	
oj39104	1500703	Human		3'		AA886687		Aorta	
GEN-288A05		Human		3'	D57248			NCI CGAP_Kid3	
vc30a07	776052	Mouse	pT7T3D	3'	AA276025			Aorta	
vu08t03	1180061	Mouse		3'	AA673797			Kidney, 6 wk	
vw64c01	1248576	Mouse		5'	AA960591			Myotubes	
vg45c07	864300	Mouse	pT7T3D	3'		AA759405	936	Mammary Gland, 4 wk	
md53e12	372142	Mouse		3'		AA458089		Mammary Gland, 4 wk	
mt72a07	419796	Mouse	pT7T3D	3'	W91182	W57082		Embryo, 13.5-14.5 dy	
vv53d11	1226133	Mouse	pT7T3D	5'	AA739434			Embryo, 13.5-14.5 dy	
me94t07	403237	Mouse	pT7T3D	5'				Thymus, 4 wk	
vc85b07		Mouse	pSPORT1	3'				Embryo, 13.5-14.5 dy	
mo83c06		Mouse		3'				Embryo, 11.5 dy	
UI-R-AO-al-b-03		Rat		3'	AA819240				
UI-R-EI-go-e-12		Rat		3'	AA964464			Embryo	

Fig. 3